

RESULT 5

BXA2_CLOBO

Title: US-10-527-411-50

Perfect score: 5864

Sequence: 1 MEFVNKQFNYKDPVNGVDIA.....AAETHDVYSWSFHASLPETN
1127

ID BXA2_CLOBO STANDARD; PRT; 1295 AA.

AC Q45894; P77780;

DT 23-JAN-2002, integrated into UniProtKB/Swiss-Prot.

DT 23-JAN-2002, sequence version 2.

DT 11-JUL-2006, entry version 57.

DE Botulinum neurotoxin type A precursor (EC 3.4.24.69) (BoNT/A)

DE (Bontoxilysin-A) (BOTOX) [Contains: Botulinum neurotoxin A light-

DE chain; Botulinum neurotoxin A heavy-chain].

GN Name=botA; Synonyms=atx, bna;

OS Clostridium botulinum.

OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;

OC Clostridium.

OX NCBI_TaxID=1491;

RN [1]

RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].

RC STRAIN=Type A / Kyoto-F;

RX MEDLINE=94143603; PubMed=8310180; DOI=10.1016/0923-2508(93)90004-L;

RA Willems A., East A.K., Lawson P.A., Collins M.D.;

RT "Sequence of the gene coding for the neurotoxin of Clostridium

RT botulinum type A associated with infant botulism: comparison with

RT other clostridial neurotoxins.";

RL Res. Microbiol. 144:547-556(1993).

RN [2]

RP NUCLEOTIDE SEQUENCE [GENOMIC DNA] OF 1-65.

RC STRAIN=Type A / Kyoto-F;

RX MEDLINE=97016817; PubMed=8863443;

RA East A.K., Bhandari M., Stacey J.M., Campbell K.D., Collins M.D.;

RT "Organization and phylogenetic interrelationships of genes encoding

RT components of the botulinum toxin complex in proteolytic Clostridium

RT botulinum types A, B, and F: evidence of chimeric sequences in the

RT gene encoding the nontoxic nonhemagglutinin component.";

RL Int. J. Syst. Bacteriol. 46:1105-1112(1996).

CC -!- FUNCTION: Inhibits acetylcholine release. The botulinum toxin

CC binds with high affinity to peripheral neuronal presynaptic

CC membrane to the secretory vesicle protein SV2. It binds directly

CC to the largest luminal loop of the three isoforms SV2A, SV2B and

CC SV2C. It is then internalized by receptor-mediated endocytosis.

CC The C-terminus of the heavy chain (H) is responsible for the

CC adherence of the toxin to the cell surface while the N-terminus

CC mediates transport of the light chain from the endocytic vesicle

CC to the cytosol. After translocation, the light chain (L)
 CC hydrolyzes the 197-Gln-|-Arg-198 bond in SNAP-25, thereby blocking
 CC neurotransmitter release. Inhibition of acetylcholine release
 CC results in flaccid paralysis, with frequent heart or respiratory
 CC failure (By similarity).
 CC -|- CATALYTIC ACTIVITY: Limited hydrolysis of proteins of the
 CC neuroexocytosis apparatus, synaptobrevins, SNAP25 or syntaxin. No
 CC detected action on small molecule substrates.
 CC -|- SUBUNIT: Disulfide-linked heterodimer of a light chain (L) and a
 CC heavy chain (H) (By similarity).
 CC -|- SUBCELLULAR LOCATION: Secreted protein.
 CC -|- MISCELLANEOUS: There are seven antigenically distinct forms of
 CC botulinum neurotoxin: Types A, B, C1, D, E, F, and G.
 CC -|- SIMILARITY: Belongs to the peptidase M27 family.
 CC -----
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 CC -----
 DR EMBL; X73423; CAA51824.1; -; Genomic_DNA.
 DR EMBL; X87974; CAA61234.1; -; Genomic_DNA.
 DR PIR; I40645; I40645.
 DR PDB; 1E1H; X-ray; A/C=1-249, B/D=250-415.
 DR MEROPS; M27.002; -.
 DR InterPro; IPR011591; Botulinum.
 DR InterPro; IPR008985; ConA_like_lec_gl.
 DR InterPro; IPR013320; ConA_like_subgrp.
 DR InterPro; IPR011065; Kunitz_like.
 DR InterPro; IPR006025; Pept_M_Zn_BS.
 DR InterPro; IPR000395; Peptidase_M27.
 DR InterPro; IPR013104; Toxin_rcpt_bd_C.
 DR InterPro; IPR012928; Toxin_rcpt_bd_N.
 DR InterPro; IPR012500; Toxin_trans.
 DR Pfam; PF01742; Peptidase_M27; 1.
 DR Pfam; PF07951; Toxin_R_bind_C; 1.
 DR Pfam; PF07953; Toxin_R_bind_N; 1.
 DR Pfam; PF07952; Toxin_trans; 1.
 DR PRINTS; PR00760; BONTOXILYSIN.
 DR ProDom; PD001963; Botulinum; 1.
 DR PROSITE; PS00142; ZINC_PROTEASE; FALSE_NEG.
 KW 3D-structure; Hydrolase; Membrane; Metal-binding; Metalloprotease;
 KW Neurotoxin; Protease; Toxin; Transmembrane; Zinc.
 FT INIT_MET 0 0 By similarity.
 FT CHAIN 1 447 Botulinum neurotoxin A light-chain.
 FT /FTid=PRO_0000029213.
 FT CHAIN 448 1295 Botulinum neurotoxin A heavy-chain.
 FT /FTid=PRO_0000029214.

| | | | |
|-------------|------|------|-------------------------------------|
| FT TRANSMEM | 626 | 646 | Potential. |
| FT TRANSMEM | 655 | 675 | Potential. |
| FT ACT_SITE | 223 | 223 | By similarity. |
| FT METAL | 222 | 222 | Zinc (catalytic) (By similarity). |
| FT METAL | 226 | 226 | Zinc (catalytic) (By similarity). |
| FT DISULFID | 429 | 453 | Interchain (between light and heavy |
| FT | | | chains) (By similarity). |
| FT DISULFID | 1234 | 1279 | By similarity. |
| FT TURN | 9 | 10 | |
| FT STRAND | 15 | 22 | |
| FT TURN | 24 | 25 | |
| FT TURN | 27 | 28 | |
| FT STRAND | 32 | 38 | |
| FT TURN | 39 | 40 | |
| FT STRAND | 41 | 47 | |
| FT STRAND | 50 | 51 | |
| FT TURN | 53 | 54 | |
| FT STRAND | 57 | 57 | |
| FT STRAND | 59 | 59 | |
| FT STRAND | 62 | 63 | |
| FT STRAND | 67 | 68 | |
| FT STRAND | 72 | 72 | |
| FT TURN | 74 | 77 | |
| FT STRAND | 79 | 79 | |
| FT HELIX | 80 | 98 | |
| FT TURN | 99 | 99 | |
| FT STRAND | 100 | 100 | |
| FT HELIX | 101 | 112 | |
| FT STRAND | 118 | 118 | |
| FT STRAND | 121 | 122 | |
| FT TURN | 123 | 124 | |
| FT STRAND | 125 | 127 | |
| FT TURN | 130 | 131 | |
| FT STRAND | 132 | 137 | |
| FT TURN | 139 | 140 | |
| FT STRAND | 141 | 141 | |
| FT STRAND | 143 | 147 | |
| FT STRAND | 149 | 154 | |
| FT STRAND | 157 | 158 | |
| FT TURN | 159 | 160 | |
| FT STRAND | 163 | 165 | |
| FT STRAND | 167 | 168 | |
| FT TURN | 171 | 172 | |
| FT TURN | 174 | 176 | |
| FT STRAND | 177 | 178 | |
| FT STRAND | 183 | 186 | |

| | | |
|-------------|---|-----|
| FT TURN | 189 | 190 |
| FT STRAND | 191 | 197 |
| FT STRAND | 210 | 213 |
| FT HELIX | 216 | 231 |
| FT TURN | 232 | 233 |
| FT TURN | 238 | 239 |
| FT STRAND | 241 | 245 |
| FT STRAND | 253 | 258 |
| FT HELIX | 259 | 265 |
| FT HELIX | 267 | 272 |
| FT STRAND | 273 | 273 |
| FT HELIX | 275 | 298 |
| FT STRAND | 301 | 302 |
| FT STRAND | 304 | 307 |
| FT HELIX | 309 | 320 |
| FT TURN | 321 | 321 |
| FT STRAND | 323 | 324 |
| FT TURN | 326 | 327 |
| FT STRAND | 328 | 328 |
| FT STRAND | 330 | 331 |
| FT HELIX | 334 | 346 |
| FT TURN | 347 | 347 |
| FT STRAND | 348 | 348 |
| FT HELIX | 350 | 357 |
| FT TURN | 358 | 358 |
| FT STRAND | 363 | 365 |
| FT STRAND | 372 | 374 |
| FT STRAND | 378 | 379 |
| FT TURN | 380 | 382 |
| FT STRAND | 384 | 384 |
| FT TURN | 385 | 387 |
| FT STRAND | 388 | 388 |
| FT TURN | 389 | 389 |
| FT TURN | 395 | 396 |
| FT STRAND | 397 | 398 |
| FT TURN | 399 | 400 |
| FT HELIX | 401 | 403 |
| FT STRAND | 404 | 404 |
| FT TURN | 405 | 408 |
| FT HELIX | 409 | 411 |
| FT STRAND | 413 | 414 |
| SQ SEQUENCE | 1295 AA; 149280 MW; 5DA04A13D98D6372 CRC64; | |

Query Match 70.6%; Score 4140; DB 1; Length 1295;

Best Local Similarity 90.9%; Pred. No. 3.2e-196;

Matches 790; Conservative 36; Mismatches 43; Indels 0; Gaps 0;

Qy 3
FVNKQFNYPVNGVDIA YIKIPNAGQM QPVKAFKIHNKIWVIPERDTFTNPEEG
DLNPP 62

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Db 2
FVNKQFNYPVNGVDIA YIKIPNAGQM QPVKAFKIHNKIWVIPERDTFTNPEEG
DLNPP 61

Qy 63
PEAKQVPVSYDSTYLSTDNEKDNYLKGVTKLFERIYSTDLGRMLLTSIVRGIPF
WGGST 122

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Db 62
PEAKQVPVSYDSTYLSTDNEKDNYLKGVTKLFERIYSTDLGRMLLTSIVRGIPF
WGGST 121

Qy 123
IDTELKVIDTNCINVIQPDGSYRSEELNLVIIGPSADIIQFECKSFGHEVLNLTRNGY
GS 182

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Db 122
IDTELKVIDTNCINVIQPDGSYRSEELNLVIIGPSADIIQFECKSFGHDVLNLTRNGY
GS 181

Qy 183
TQYIRFSPDFTFGFEESLEVDTNPLL GAGKFATDPAVTLAHELHAGHRLYGIAIN
PNRV 242

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Db 182
TQYIRFSPDFTFGFEESLEVDTNPLL GAGKFATDPAVTLAELHAHRLYGIAINP
NRV 241

Qy 243
FKVNTNAYYEMSGLEVSFEELRTFGGHDAKFIDSLQENEFRLYYYNKFKDIASTL
NKAKS 302

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Db 242
FKVNTNAYYEMSGLEVSFEELRTFGGHDAKFIDSLQENEFRLYYYNKFKDVAST
LNKAKS 301

Qy 303
IVGTTASLQYMKNVFKKYLSEDTSGKFSVDKLFKLYKMLTEIYTEDNFVK
FFKVLN 362

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Db 302
IIGTTASLQYMKNVFKEKYLLSEDTSGKFSVDKLKFDKLYKMLTEIYTEDNFVNF
FKVIN 361

Qy 363
RKTYLNFDKAVFKINIVPKVNYTIYDGFNLRNTNLAANFNGQNTTEINNMNFTKL
KNFTGL 422

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Db 362
RKTYLNFDKAVFRINIVPDENYTIKDGFNLKGANLSTNFNGQNTTEINSRNFTRLK
NFTGL 421

Qy 423
FEFYKLLCVRGIHITSKTKLVPRGSNKALNDLCIKVNNWDLFFSPSEDNFTNDLNK
GEEIT 482

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Db 422
FEFYKLLCVRGIHPFKTKSLDEGYNKALNDLCIKVNNWDLFFSPSEDNFTNDLDK
VEEIT 481

Qy 483
SDTNIEAAEENISLDLIQQYYLTFNFDNEPENISIENLSSDIIGQLELMPNIERFPNGK
K 542

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Db 482
ADTNIEAAEENISLDLIQQYYLTFDFDNEPENISIENLSSDIIGQLEPMPNIERFPNG
KK 541

Qy 543
YELDKYTMFHYLRAQEFEGHKSRIALTNSVNEALLNPSRVYTTFFSSDYVKKVVK
ATEAAM 602

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Db 542
YELDKYTMFHYLRAQEFEGHGSRIILTNSAEEALLKPNVAYTTFFSSKYVKKINKA
VEAFM 601

Qy 603
FLGWVEQLVYDFTDETSEVSTTDKIADITIIPYIGPALNIGNMLYKDDFVGALIFS
GAV 662

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Db 602
FLNWAEELVYDFTDETNEVTTMDKIADITIIPYIGPALNIGNMLSKGEFVEAIIFT
GVV 661

Qy 663
ILLEFIPEIAIPVLGTFALVSYIANKVLTQIDNALS KRNEKWDEVYKYIVTNWL
AKVN 722

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Db 662
AMLEFIPEYALPVFGTFAIVSYIANKVLTQINNALS KRNEKWDEVYKYTVTN
WLAKVN 721

Qy 723
TQIDLIRKKMKEALENQAEATKAIINYQYNQYTEEEKNNINFNIDDLSSKLNESIN
KAMI 782

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Db 722
TQIDLIREKMKKALENQAEATKAIINYQYNQYTEEEKNNINFNIDDLSSKLNESIN
SAMI 781

Qy 783
NINKFLNQCSVSYLMNSMIPYGVKRLED F DASLKDALLKYIYDNRGTLIGQVDR
LKDKVN 842

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Db 782
NINKFLDQCSVSYLMNSMIPYAVKRLKDFDASVRDVLLKYIYDNRGTLVLQVDR
LKDEVN 841

Qy 843 NTLSTDIPFQLSKYVDNQRLSTFTEYIK 871

||| |||||:|||||||

Db 842 NTLSDIPFQLSKYVDNKKLLSTFTEYIK 870